

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:03:35 ; Search time 157.73 Seconds  
(without alignments)  
2217.642 Million cell updates/sec

Title: US-09-540-235-1

Perfect score: 408  
Sequence: 1 acgcgcgcgatgagatta.....acatccatcatatgttgta 408

Scoring table:  
IDENTITY\_NNC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_1101:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	130	31.9	637	21 AAC49069	Arabidopsis thalia
2	124.2	30.4	636	21 AAC45801	Arabidopsis thalia
3	121	29.7	638	21 AAC34600	Arabidopsis thalia
4	118	28.9	638	21 AAC38634	Arabidopsis thalia
5	109.8	26.9	1348	22 AAH29927	C albicans apoplos
6	104.2	25.5	496	21 AAA31256	Plant microsateilli
7	102.2	25.0	788	21 AAF08074	Fusarium venenatum
8	101.2	24.8	431	22 AAF02287	Probe #20973 used
9	97.6	23.9	747	21 AAF12354	Aspergillus oryzae
10	95.8	23.5	1331	22 AAC29813	S cerevisiae apoplo
11	90.4	22.2	508	21 AAC03878	Human secreted pro

12	87.8	21.5	785	21 AAF15011	Trichoderma reesei
13	80.6	19.8	472	22 AA139236	Probe #7922 used t
14	74.6	18.3	450	21 AAC41333	Zea mays DNA fragm
15	73.4	18.0	629	21 AAF13388	Aspergillus niger
16	71.4	17.5	579	21 AAF1407	Aspergillus niger
17	70.4	17.3	358	21 AAC00996	Human secreted pro
18	63.2	15.5	258	22 AA125954	Probe #15887 for g
19	63.2	15.5	258	22 AA153325	Probe #22011 used
20	63.2	15.5	505	22 AA116759	Probe #6692 for ge
21	63.2	15.5	505	22 AA140246	Probe #8932 used t
22	57.8	14.2	300	22 AA121431	Probe #11364 for g
23	57.8	14.2	300	22 AA146720	Probe #15406 used
24	57.8	14.2	300	22 AA107126	Probe #7117 used t
25	51	12.5	449	22 AAH83347	Human ovarian tumo
26	48.2	11.8	936	22 AAF58252	Oligonucleotide D1
27	48.2	11.8	936	22 AAF58254	Oligonucleotide D1
28	48.2	11.8	936	22 AAF58257	Oligonucleotide D1
29	48.2	11.8	936	22 AAF58259	Oligonucleotide D1
30	48.2	11.8	936	22 AAF58262	Oligonucleotide D1
31	48.2	11.8	936	22 AAF58265	Oligonucleotide D1
32	47.4	11.6	305	21 AAC18519	Human secreted pro
33	47.4	11.6	936	22 AAF58252	Oligonucleotide D1
34	47.4	11.6	936	22 AAF58254	Oligonucleotide D1
35	47.4	11.6	936	22 AAF58257	Oligonucleotide D1
36	47.4	11.6	936	22 AAF58259	Oligonucleotide D1
37	47.4	11.6	936	22 AAF58262	Oligonucleotide D2
38	47.4	11.6	936	22 AAF58265	Oligonucleotide D2
39	45	11.0	205	21 AAA31734	Plant microsateilli
40	44.8	11.0	465	22 AA112233	Probe #2166 for ge
41	44.8	11.0	465	22 AA133587	Probe #2273 used t
42	44.8	11.0	465	22 AA102146	Probe #2137 used t
43	44.6	10.9	287	15 AA076714	Human genome fragm
44	44	10.8	199	21 AAC10159	Human secreted pro
45	43	10.5	337	21 AA280502	Human colon cancer

#### ALIGNMENTS

RESULT 1

AAC49069 standard; DNA: 637 BP.

XX AAC49069;

XX

DT 18-OCT-2000 (first entry)

XX

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 59811.

XX

XX Hybridisation assay; genetic mapping; gene expression control;

KW Protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

XX Arabidopsis thaliana.

XX

XX EP1033405-A2.

XX

PD 06-SEP-2000.

XX

XX 25-FEB-2000; 2000EP-0301439.

XX

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

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PR 19-APR-1999; 99US-0130077.

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Db 91 caattcacagctcccttcgaagcgttgagcgcttcacatgagctgcgcgttataccaagct 150  
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QY 387 atacatccatcaatgtgtta 408  
Db 331 gtcaatgcttcgaatgtgatga 352

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AC AAC45801;  
XX 18-OCT-2000 (first entry)  
DT 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 47813.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47813.  
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XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
PN EP1033405-A2.  
XX 06-SEP-2000.  
PD 06-SEP-2000.  
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PR	31-AUG-1999.	990S-0151438.
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PR	10-SEP-1999.	990S-0153070.
PR	13-SEP-1999.	990S-0153758.
PR	15-SEP-1999.	990S-0154039.
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PR	22-SEP-1999.	990S-0155486.
PR	24-SEP-1999.	990S-0155658.
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PR	29-SEP-1999;	9905-01565596
PR	04-OCT-1999;	9905-01571717
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Dd		178	aagttcaatgtccatgccatgtccgataccgttaaaagacgcagaggtctcagatcgtttcgtgtc	237
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Dd		298	atcgcagaaatcatcacgagygagaaagtgtaatvgaacacacgcgtggaatltcagtcgcg	357
OY		396	tctaatgtgttta	408
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XX		AC	AAC34600;	
XX		DT	17-OCT-2000 (first entry)	
XX				

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7218.  
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XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
XX  
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PD 06-SEP-2000.  
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PR 28-OCT-1999; 99US-0161920.
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Query Match 29.7%; Score 121; DB 21; Length 638;

Best Local Similarity 61.7%; Pred. No. 8.4e-29;

Matches 193; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

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QY 336 atcgagagagtgacgcaggaagaaagcgaatggaatgactgcttggtggaatacatca 395
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21687.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
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PD 06-SEP-2000.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
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PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR:
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID NO 20973; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 431 BP; 75 A; 107 C; 110 G; 139 T; 0 other;
XX
Query Match 24.8%; Score 101.2; DB 22; Length 431;
Best Local Similarity 59.3%; Pred. No. 1.5e-22;
Matches 191; Conservative 0; Mismatches 128; Indels 3; Gaps 1;
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DB 363 ttcaatgcccctccacacgtgcgagaaagatcatgctatccctctccaaagagcgtg 304
QY 210 cgtacgaataagagtgctgtcttcttaccatctgaaagaagaagaaatcatcagtt 269
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QY 270 cgcgagccttcaaggtgagagaa---ggaaaaagttacaagtgatcgcgaagaagaat 326
DB 243 cgcgagcactacaaagcgtcagcaaaattggcagaagatccagctgacagaaagaaatxt 184
QY 327 cggatacatatcgagagagtgaccagagaagaagcgaatgagatgactgtactctgtgga 386
DB 183 gtcatctacatcgagcgggtgcagcctgagaaagccacgacgactgtccacggtggcc 124
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RESULT 9
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XX 13-MAR-2001 (first entry)
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XX Multiple gene expression; filamentous fungal cell; EST;
XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX culture condition; environmental stress; spore morphogenesis;
XX metabolic pathway engineering; catabolic pathway engineering; ss.
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XX Aspergillus oryzae.
XX
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PN WO200056762-A2.
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XX 28-SEP-2000.
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XX 22-MAR-2000; 2000MO-US07781.
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XX 22-MAR-1999; 99US-0273623.
XX
XX (NOVO ) NOVO NORDISK BIOTECH INC.
XX (NOVO ) NOVO NORDISK AS.
XX
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB:
XX WPI; 2000-594572/56.
XX
XX Monitoring differential expression of genes in filamentous fungal cells
XX uses fluorescence-labeled nucleic acids isolated from the cells and a
XX substrate of expressed sequence tags -
XX
XX Claim 88; Page 2058; 3161bp; English.
XX
XX The present invention describes a method for monitoring differential
XX expression of genes in a first filamentous fungal (FF) cell relative to
XX expression of the same genes in one or more second filamentous fungal
XX cells. The method uses fluorescence-labeled nucleic acids isolated from
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs
XX are used in the methods for monitoring differential expression of genes
XX in a first filamentous fungal (FF) cell relative to expression of the
XX same genes in one or more second filamentous fungal cells. Monitoring
XX the global expression of genes from FF cells allows the production
XX potential of the microorganisms to be improved. New genes may be
XX discovered, possible functions of unknown open reading frames can be
XX identified and gene copy number variation and stability can be
XX monitored. The expression of genes can be used to study how FF cells
XX adapt to changes in culture conditions, environmental stress, spore
XX morphogenesis, recombination, metabolic or catabolic pathway
XX engineering. Using ESTs provides several advantages over genomic or
XX random cDNA clones including elimination of redundancy as one spot on an
XX array equals one gene or open reading frame, and organisation of the
XX microarrays based on function of the gene products to facilitate
XX analysis of the results. AAF07478 to AAF11247 represents ESTs from
XX Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
XX niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
XX AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
XX all specifically claimed in the present invention.
XX
Sequence 747 BP; 175 A; 210 C; 196 G; 166 T; 0 other;
XX
Query Match 23.9%; Score 97.6; DB 21; Length 747;
Best Local Similarity 58.1%; Pred. No. 2.5e-21;
Matches 172; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
QY 113 tgtatcgtcgtctgaagaagcagaggaagaacatcttaacgacacatctctgtacg 172
DB 78 ttggccctctcccgcggaagtcgcgcaagcgacattcaacgttgctccgcgagcg 137
QY 173 acgaatactcatgagtgacacctgtgtccaaagaaactagctagaataacagcggtctc 232
DB 138 ccgtgtcatcatgagcgcctcttgagcaagaactccgtggaagtacatcgtccgctc 197
QY 233 ttaccctattcgaaagaagacgaatcatatgcttcgcgagccttcaagggtagaaga 292
DB 198 tctcccatcgcgaagcagcagagtgatcatctgtccgtgagcagaaggcgcgtga 257
QY 293 aggaagaattcaacggtgttctcgaaagaatatcgatcatatcgagagatgacacag 352
DB 258 gggcagaatcaccaacgcttaccgcttaagtgggttctcagcgtcgcgctgcgcgcg 317
QY 353 aaaaaaacgaatggaatgactgtactctgttggaaatatacatcatcctaattgttta 408
DB 318 cgagaagtcacaacgcgccagagcgttccctcgtatccaccctcccaagtcgtca 373
```



Db 248 cactataaaggtcagcaaatgtgcgaagtgtccagglttaccaggaataatggtatc 307  
Oy 333 catctcgagaagtgaccacagagaacgcgaatggaatgactgtgactgtggaatacat 392  
Db 308 tacattgacggggtgcgcgggaaaggctaatgtgcacaactgtccacgtgacattcac 367  
Oy 393 ccatctaattgtgtta 408  
Db 368 ccagcaaggtgttta 383

RESULT 12  
AAFI5011  
ID AAF15011 standard; CDNA: 785 BP.  
AC AAF15011;  
XX 13-MAR-2001 (first entry)  
XX Trichoderma reesei EST SEQ ID NO:7534.  
DE  
XX Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.  
OS Trichoderma reesei.  
XX WO200056762-A2.  
XX 28-SEP-2000.  
XX 22-MAR-2000; 2000WO-US07781.  
XX 22-MAR-1999; 99US-0273623.  
XX (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
PI WPI: 2000-594572/56.  
XX Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags -  
XX Claim 89; Page 3043; 3161pp; English.

CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random CDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus  
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and

CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are  
CC all specifically claimed in the present invention.  
XX  
SQ Sequence 785 BP; 187 A; 229 C; 193 G; 156 T; 20 other:  
Query Match 21.5%; Score 87.8; DB 21; Length 785;  
Best Local Similarity 58.5%; Pred. No. 3.4e-18;  
Matches 169; Conservative 0; Mismatches 119; Indels 1; Gaps 1;  
Oy 115 tctcgtctctatagaagaacagagaacatacttcaagcacattcttctgtcagc 174  
Db 25 ttctctctccgagcaagacagcgtgcctcacttcaagcgcggctgcgcagcc 84  
Oy 175 gaatacctcagaatgacaccttggtccaaggaactgaactgaataacagcgtgtctt 234  
Db 85 gtgtcattcagtcgcgtccctttagcaagagctgcgcgagaagtacaacglttcgacga 144  
Oy 235 tactattcgaagaagacgaagtaatacattatctgcgcgagcttcaagggtagaagaag 294  
Db 145 tcccatccgcaagagacgaagaggtcacatctgtcgttgcgtccacaagggcgtgag 204  
Oy 295 gaaagttacaacgtgttatcgaaagaataatcggatacatatcgaagaagtgaccag 354  
Db 205 gcaaggtcaccttcgtctaccgcctcaagtaacgttgatccacgltcgcgttaccgcg 264  
Oy 355 aaaaagcgaatgaaatgactcctgtgggaatacatcatcaatgt 403  
Db 265 acaagccacgagccagacgctncc-ctgggtatccacccctccacgt 312

RESULT 13  
AAI39236/c  
ID AAI39236 standard; DNA: 472 BP.  
XX  
AC AAI39236;  
XX 17-OCR-2001 (first entry)  
XX  
DE Probe #7922 used to measure gene expression in human placenta sample.  
XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder; ss.  
XX Homo sapiens.  
OS  
XX WO200157272-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US00663.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.  
XX 03-AUG-2000; 2000US-0632386.  
XX 21-SEP-2000; 2000US-0234687.  
XX 27-SEP-2000; 2000US-0236359.  
XX 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI: 2001-488897/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human placenta -  
XX Claim 25; SEQ ID No 7922; 654pp; English.  
XX The present invention relates to single exon nucleic acid probes (SENP).  
XX The present sequence is one such probe. The probes are useful for

CC Producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders.  
XX  
SQ Sequence 472 BP; 105 A; 119 C; 100 G; 148 T; 0 other;

Query Match 19.8%; Score 80.6; DB 22; Length 472;  
Best Local Similarity 62.3%; Pred. No. 5.5e-16;  
Matches 144; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 181 tctgtgtcacccttgcgaaggaactcgtacgaagaacgcttcttactcta 240  
468 TCATGTCATCCCGCTCTCCAGAGACTCGGCAGAGTACATGCTCCCTCATGCCCA 409  
QY 241 ttccgaagaagcagaatcatcattcgcggagcttcaaggtagaaga---gga 297  
408 TCCGCAGAGACGACGAGGTCCAGGTGATCGAGACACTACAAAGGTCCAGAAATTGGCA 349  
QY 298 aagttacaacgtgttatacgaagaataatcgatacatatcagagagatgaccagagaa 357  
348 AGTATATCCAGGTGTACAGAAAGAAATATGTCATCATCTCAGCGGGTCCAGCTGAGA 289  
QY 358 aagcgaatggaatgactgttactctgtgggaatacatcatcctaattgttga 408  
288 AGGCCAAGCGCAGACTGTCTCAGTGGGCAATTCACCCAAAGCAAGGTGTTA 238

## RESULT 14

ID AAC41333 standard; DNA; 430 BP.  
XX AAC41333;

DT 17-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 31502.

KW Hybridisation assay; genetic mapping; gene expression control;  
KW Protein identification; signal transduction pathway; metabolic;  
XX pathway; promoter; termination sequence; corn; ss.

OS Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126284.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139889.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.



XX Claim 87; Page 1742-1743; 3161pp; English.  
PS  
XX

CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
CC same genes in one or more second filamentous fungal cells. Monitoring  
CC the global expression of genes from FF cells allows the production  
CC potential of the microorganisms to be improved. New genes may be  
CC discovered, possible functions of unknown open reading frames can be  
CC identified and gene copy number variation and stability can be  
CC monitored. The expression of genes can be used to study how FF cells  
CC adapt to changes in culture conditions, environmental stress, spore  
CC morphogenesis, recombination, metabolic or catabolic pathway  
CC engineering. Using ESTs provides several advantages over genomic or  
CC random cDNA clones including elimination of redundancy as one spot on an  
CC array equals one gene or open reading frame, and organisation of the  
CC microarrays based on function of the gene products to facilitate  
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from  
CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from *Aspergillus*  
CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and  
CC AAF14879 to AAF15337 represents ESTs from *Trichoderma reesei*, which are  
CC all specifically claimed in the present invention.  
XX

Sequence 629 BP; 153 A; 191 C; 155 G; 129 T; 1 other;

Query Match 18.0%; Score 73.4; DB 21; Length 629;

Best Local Similarity 54.7%; Pred. No. 1.2e-13;  
Matches 146; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 113 tgtatcgtcgtctagaagaagcagaggaagaaacattcaagcaccatctctgtacg 172  
DB 70 tctcgccctcttcgcgcgaagtcgcgcgccaccattcaagccctccagcagcg 129  
QY 173 acgaatactcatgtagcaccctgtccaagaaactagctgaataatcagcttcgtc 232  
DB 130 ccgcgttatctctctcctctctcgcgagctccgcgcgaatataatgtccgtc 189  
QY 233 ttactcattcgaaagaagaagaagatataatcgttcgagagcttcaaggtagaga 292  
DB 190 catgccatccgcagagcagcgatgcatgtcgtgcagcaacaaggcgctga 249  
QY 293 aggaagaatcacaacgtttatcgaagaataatcgtatataatcgaagagtgaccag 352  
DB 250 gggcagaagtcacccgcgtctacccgttaagtggtgcacatccagctcgagcagcg 309  
QY 353 agaaagcgaatggaatgactgtacc 379  
DB 310 cgacaagagcaagcgccagagcgtccc 336

Search completed: March 2, 2002, 20:31:37  
Job time: 1682 sec

